

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Kriz, Alan L.

Luethy, Michael H.

Voyles, Dale A.

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF
TRANSGENES IN PLANTS

(iii) NUMBER OF SEQUENCES: 28

(iv) CORRESPONDENCE ADDRESS:

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- (C) CITY: Houston
- (D) STATE: TX
- (E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US Unknown
- (B) FILING DATE:
- (C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Highlander, Steven L.

(B) REGISTRATION NUMBER: 37,642
(C) REFERENCE/DOCKET NUMBER: DEKM:158

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGGAACCTGG AACGGGCTTG GA

22

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGAGGGCAA CGAGGCAGCAC CTTCATGG

28

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTAATACGAC TCACTATAGG GC

22

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTATAGGGC ACGCGTGGT

19

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCTCGAGGG ACCGGTTACA GCACACCACT G

31

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGTCTAGAGG TGTGATCTT CTGTGCTCT

29

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCCATGGGG TGTGATCTT CTGTGCTCT

29

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGACCGGTTA CAGCACACCA CTGTGGTGG TCTCAAGGCA GTACCAAAC	60
TATAGCAGCA GAATCACCTG TCTTGTCTAC AAGACAGAAC CAATGCATCA ACTTCAAGGG	120
AGTACCAGCG TCTTCTTGAC TGTCTTCAG AATTGTGGCA TTCTTGTGG AAGCATAGCA	180
GTGTAGGTTG CTCATTCACG GATAATCTCG ACACGTAAG TGATGAGGAA TACGGAACGA	240
CCATTGGCAT GTAGAGCTGT ATGAATTGGT GTTATCCATA CAACAACTCG CAGAACATCA	300
CAAAATTGCA CGTCAATGGA TTGGGTCAGA AACAAATCGT CTCCTTGTAG CTTGTACAAT	360
GAAGTGATGG TGAGTCATGA GTCACACTGA TCCGATCTGA TATATATGCC AAATAGCTCA	420
CACGACAACA TTACAAACAA CCCCATACTA TACATCACAA AGTTTGTTC ATGAAAAAAC	480
AAATAAGTAT GCAGGAGGGG ACAATAATCC TTGCTTGACG CGTAAAGTGA ATTTACAAAG	540
CCATATATCA ACCTATATCT AATTAATAAG TTCGTTATAT ATACGCACGA TGATCATCAA	600
CAACCGTACC TGTGAAAGGC AACAAAATGA GCCACGCAA AATGCAGAAT GAATCCATAT	660
GATGACGAAC GTACACTCGG CTTGCTACAT AAAGTGAATG ATGAGTCATA AATATTTGGC	720
AAGAAACCGT GAAAGCTACA CAGCCGTCGT CAGTAGCACA GGAACACAAAG AAACGTGCT	780
AATCGAAGCT ATAAATAACC CTAGTATGCC TATGCACTTC TCCATCACCA CTACCCATAT	840
CTTCAGTCTA TTTACCTTCT CTATCTACTC CAGAGAGCAC AGAAGATCGA CACC	894

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCAGCCCCA GCAGCCACAT CCA

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGCGGCAGC CAATGACAAG TC

22

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACTGAAGAAA CTATATCCTA CTGTAATAAT AATGATGTAA TATAGCCGCT GGCGAGCTAA	60
GCTAGTTTAG TCATTTAGCG CGGCGATGGG TAATAAAAGT GTCATCCATC ACCATGGGTG	120
ACAATATATG CGAACAAATG ACCTGAAGAT GAACAATTGA AATGAAAAGG AAAATATATT	180
ACAATTCAAC GAGATATCCT CTCGATCGTA TCACGTGTCC ACAGGGGTGG ATCCATGCC	240
CGGGCTGCC CGGCTGCAGC CCGGGCGTA GACCAAAAAT CCCTTAGCG ATTCTTTTT	300
TCAGTTCAAT TTTGCCAATA AAAACTACAT TTAGCCCTAC CTGATGCGGT CTAAAATTT	360
TTTACACTAG TTTAGCCCT CCTGTAATGT GTTTCTAGAT CAGGCAATGT AT	412

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCTCGAGGG ACCGGTTACA GCACACCACT G	31
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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCAGTACTGG GCACCGCCGG C

21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AAGGTGCTGC TCGTTGCCCT C

21

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGAGCTCTC AGTACTGGGC ACCGCCGGC

29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGAAGGTGC TGCTCGTTGC CCTCGCTCTC CTGGCTCTCA CTGCGAGCGC CACCTCCACG	60
CAAATAGGCG GCACGTGCGG CTGCCAACCA CCGCATCTGC CACCGCCGCC GGTTCATCTG	120
CCGCCTCCGG TTCACCTGCC CCCGCCGGTT CATCTGCCGC CGCCACAATG CCACTACCCT	180
ACTCAACCGC CCCGGCCTCA GCCCCAGCAG CCACATCCAT GCCCATACCA ACCGCAGCAT	240
CCAAGCCCGT TCCAGTTCCA GCAGCCGGGA ACCTGCGTTG GCCAAGGCAC CCAGATCCTG	300
GGCCAGTGCA TTGAGTTCCCT GAGGCATCAG TGCAAGCCGG CGGCGACGCC CTACTGCTCG	360
CCACAATGCC AGGCAGTTGCG GCAGCAGTGT TGCCACCAGC TCAGGCAGGT GGAGCCGCTG	420
CACCGGCAAC AGGCAGATCTT CGGCGTGGTC CTGCAGTCCA TCCAGCAGCA GCCGATAGGC	480
CAGCCGCTCG CGGCAGTGAT GGCGCGCAA ATAGCGCAGC AACTGACGGA GATGTGCGGT	540
GTGCGGCAGC CAATGACAAG TCCCTGCCCT TGCAAGCGCTG CTGCCGGCGG TGCCCAAGTAC	600
TGA	603

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGAAGAAGCA CGTACGCGGG CGGAACGCGT GTCCTGCCTG GATACCGCGC GCGAGATGAC	60
GTGCGGCCGGC GGCGCGCGAC TACCGCCGGC GCGGCATGGC CCTACTACGG CGGCTGCTGC	120
TGCTGCTACG TACGCTGCCG TAAAGTCTCG GTCGCCGTGC TAGCTCTAGC TAGTCGTTAT	180
GTGTGTTGTG CTTTGTATGT GCGCGTGTCT TGTTGGGACA TGCAGTGTAG TGCTGCTGTA	240
TGCGTGTGTC CTTTCTTGAT CGGAGTCGGA GTGGCTGATG CACAGCATGC TGGATGTCAA	300
GTTTATGATG AGGAATAAAA TGCAATGTTCA AGGGCGAGAT ACTACGGTTT TCCTTGACTA	360
CCATGGGATT TGTAGAA	377

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCACTCGGCT TGCTACATAA AGTGAATGAT GAGTCATAAA TATTGGCAA GAAACCGTGA	60
AAGCTACACA GCCGTCGTCA GTAGCACAGG AACACAAGAA ACTGTGCTAA TCGAAGCTAT	120
AAATAACCCT AGTATGCCTA TGCACTTCTC CATCACCACT ACCCATATCT TCAGTCTATT	180
TACCTTCTCT ATCTACTCCA GAGAGCACAG AAGATCGACA CC	222

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTAAGTATGC AGGAGGGAC AATAATCCTT GCTTGACGCG TAAAGTGAAT TTACAAAGCC	60
ATATATCAAC CTATATCTAA TTAATAAGTT CGTTATATAT ACGCACGATG ATCATCAACA	120
ACCGTACCTG TGAAAGGCAA CAAAATGAGC CACGCAAAAA TGCAGAATGA ATCCATATGA	180
TGACGAACGT ACACTCGGCT TGCTACATAA AGTGAATGAT GAGTCATAAA TATTGGCAA	240
GAAACCGTGA AAGCTACACA GCCGTCGTCA GTAGCACAGG AACACAAGAA ACTGTGCTAA	300
TCGAAGCTAT AAATAACCCT AGTATGCCTA TGCACTTCTC CATCACCACT ACCCATATCT	360
TCAGTCTATT TACCTTCTCT ATCTACTCCA GAGAGCACAG AAGATCGACA CC	412

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATCGAGACA AGCACGGTCA ACTTC

25

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGTCCCTGG AGGCACAGGG CTTCAAGA

28

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TATGAATTAT TATGTATTAA TTAATTTCAGTCGATTAA AAAATAAAAG AAAAGTAAAT	60
TGGAGATTTT ACATTGGAA CCTAGAAAAT TTTTATTAACTTTCTCTCT TCCATCGTAA	120
CGATTCTGGG CTGATTGGGC CTACAGAGAG GAGAGCGAAA GCGAAGTAAT ATGAGATTAA	180
ACATTAGGAA CCCTAGAATA TTTTTTATTAACTTTCTCTCT CTTCTAGAAA AGTTGGATGG	240
AGGAGGCCAT CGGTAAACCG AACACGGACA AGATCAGGGG CAAAAGAAAA TATTGGCAA	300
ACTAAAATTT TGGCTCTTAA TAGATAGGTA TAGATTGGG TTAAGAACAG TAGTCGGACA	360
TTCCACGCTT TGTTAAGTTC TTTTTTACA TAACAAGAAT AGAACATCACGC TCTGTAGGCT	420
CGTCAGACCG TACCTTCTA AGGAAGTCGC TTTGGTAGT TCAGTTGGCG AGAAAAGCCT	480
TCCCTACCTTT GCAGGTCCAT CGGGCCGACT ACAACCCGTG GCTCAATCCC GGTTCTTGCG	540
GTGTCTTGGC AACATTCTTG TTGGAAGATA CCAGAAGGTT GCTCCACGGG TAATCTTGAC	600
ACGTATGTAA AGTGATGAGG AACATTGAAC GAACATTGGC ATGTAAGCTC TATAATTGGT	660
GTTATCCATA ACAACGTCGC AGAACATCAC AAATTGCACG TCAAGGGATT GGGTCAGAAA	720
CAAATCGTCT CCGTGTACAA CGAAGTGGTG AGTCATGAGC CATGTTGATC TGATATATAC	780
ATAGCACACA CGACATCACA AACAAAGTCAT ACTACATTAC AGAGTTAGTT TCACCTTCA	840
AGTAAAACA AAGTAGGCCG GAGAGAGGAC AATAATCCTT GACGTGTAAA GTGAATTAC	900
AAAGCCATAT ATCAATTAT ATCTAATTGTTTCTATGTAG ATATCAACAA CCTGTAAAAG	960
GCAACAAATT GAGCCACGCA AAATTACAAG TGAGTCCAAA TAAACCCCTCA CATGCTACAT	1020

AAAAGTGAAT GATGAGTCAT GTATATCTGG CAAGAAACTG TAGAAGCTAC AGTCATCGGT	1080
AGCAAAGAAA CACAAGAAAA TGTGCTAATA AAAGCTATAA ATAACCCTCG TACGCCTATG	1140
CACATCTCCA TCACCACCAAC TGGTCTTCAT TCAGCCTATT AACTTATATC TATCTACTCC	1200
AGAGCAGACA AGAACTCGAC ACCATGAAGG TGTTGCTCGT TGCCCTCGCT CTCCTGGCTC	1260
TCGCGAGCGC CGCCTCCACG CTTACAACCG GCGGCTGCGG CTGCCAGACA CCTCATCTAC	1320
CACCACCGCC GGTCATCTG CCGCCGCCGG TGCATCTGCC ACCGCCGGTG CACCTGCCGC	1380
CGCCGGTTCA CGTGCCACCG CCGCCACCAC AATGCCACCC ACACCCTACT CTACCGCCCC	1440
ACCCACATCC ATGCGCTACA TACCCACCGC ATCCAAGCCC GTGCCACCCA GGGCATCCCG	1500
GATCCTGCGG TGTTGGCGGC GGCCCCGTCA CCCCCGCGAT CCTGGGCCAG TGCATCGAGT	1560
TCCTGAGGCA TCAGTGCAGC CCGGCGGCGA CGCCCTACTG CTCGCCACAG TGCCAGGCGT	1620
TGCGGCAGCA GTGCTGTCAG CAGCTCAGGC AGGTGGAGCC GCTGCACCGG TACCAGGCGA	1680
TCTTCGGCGT GGTCCTGCAG TCCATCCAGC AGCAGCAGCC GCAAGGCCAG TCGTCACCGC	1740
TCCCGGCGCT GATGGCGCG CAAATAGCAC AGCAACTGAC GGCGATGTGC GGTCTAGGAG	1800
TGGGGCAGCC AAGTCCCTGC GCTTCTTGCA GCCCTTTGC CGGTGGTGTG CACTATTAAA	1860
GAAACTATCT ATACTGTAAT AATGTTGTAT AGCCGCCGGA TAGCTAGCTA GTTAGTCATT	1920
CAGCGGCGAT GGGTAATAAT AAAGTGTCA CCATCCATCA CCATGGGTGG CAACGTGAGC	1980
AATGACCTGA TTGAACAAAT TGAAATGAAA AGAAGAAATA TGTTATATGT CAACGAGATT	2040

TCCTCATAAT GCCACTGACA ACGTGTGTCC AAGAAATGTA TCAGTGATAC GTATATTCAC	2100
AATTTTTTTA TGACTTATAC TCACAATTG TTTTTTTACT ACTTATACTC GAACAATTG	2160
TTGTGGGTAC CATAACAATT TCGATCGAAT ATATATCAGA AAGTTGACGA AAGTAAGCTC	2220
ACTCAAAAAG TTAAATGGGC TGCGGAAGCT GCGTCAGGCC CAAGTTGGG CTATTCTATC	2280
CGGTATCCAC GATTTGATG GCTGAGGGAC ATATGTTCGG CTTAAGCTGC AGCTTGTAG	2340
TTAGTTTGT TTTTGATTAT ATTTAATACT CTATGCATGT GCACCAAGAT TTTCTGGTG	2400
AATTAAACAA GGCTAATAA CGTGAGTAGC GTATCTAACT GTGACCTATA AAGTAGAGCA	2460
CCTTTTTAGA GTAGGGCTC CTTTTTTAG AACTCTATT ATTGCACCCA ACTTCAATAA	2520
GGGTCTTTC ATCCAAAATT AAGAGTCCTT ACATTACATC TAATCGTCTA TTCATTGTCT	2580
ATATTTTAAT ATAAATCTTA CTGTATATCT TGTAGCACAC TAGTATGCCT CAAAGCCGAC	2640
AATAAAT	2647

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3704 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGGCGCCTG TACCGCGTGT GGGGACGATG AGCGCTCCCT GAACGCTGTC TTGGGAGAGC	60
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TGCAAGATGA GACACTCCAT CCCGCGCAGC CTGTCGTGGC GTCCTCCTGG ATGGACACCT	120
GCATCGCTGT CGCCCTCCAC CAACTCACCT GAACGAAGAA TAGAATAAAA AATGGAGGGA	180
GCTGAGGGGG CAGTGGTTGC GCTGTAGGGA GGAGAGAGAC CGCGTCATTA TAAGACTATC	240
TGCAACCGTT ACCTCTAAAT TTTTCCCTCT ATATCATTTC TTCCCCATAT TTTCCCCCT	300
ATTTTTTCAT CTCCCGCAAC GGTTTCTCCT AAATACTCCC CCTATATCTC ACTACCACTA	360
TAAAATATTA TTTTTTATAC CAACTATCAA TTTTTTATCT ACTAACAAATT ACTCGTGGAC	420
CCACAGCACA GTGTTAGGA GATGAACAGT GACACGCTAT ATCTGGGGGG AGAGAGAAAG	480
AGGCGCGCGT AGGGGGCGCG CGGTAGGGGC ACTGCTGCGG CTGTAGAGTA CCCCCTACAC	540
GCCGGCATGC AAGGGAAGGG GGCAATGTTG CGCATAGCCT AAAGAGCGGA TGAAGCGGCT	600
TGCAATTTCG ACGCTGGATT CATAAATAGT GCATATTACT AAAAAAAGGG TGGGGACGTA	660
GGTATAGAGA GTCTATTAGA GTTGATCTAA GACCCGGTTT ATTCAGATT ATAATCTGTC	720
CGGATTATAT AATCCAGCGC AAATAATACA GTAGGTAAAC AAACAACCTAG ATTATGGGTT	780
CAGATTATAT AATCTAAACC CCAGATTATG ATAATCTCAT AATCTCCTCA AGAGTAGCTT	840
ATTGGAGATT ATTTGGCAA AAGACCCACT ACCCATGGTT ATGTAAATAG AAATTATAAT	900
ATATATCATC TTTTTCTCA CCTTAAATAA ACAAAATAAGG GTATTGTTGT CTTTATGAAT	960
AATCTACATT TGTATAATCT AAACTACCAA ACAACTACAT CTAGATTATA ATCTGGATTA	1020
TATAATTAA ATTATAATCT AGATTATATA ATTTATAAGC TGAAACAAACC CGGCCCTAAA	1080
GCACATCGT ATCACCTATC TGATAGTCAC GGGTTTCGAA CGTCCACTTG CGTCGCACGG	1140

AATTGCATGT TTCTTGTGG AAGCATATTACGCAATCTCACACATAAA GGTTTATGTA	1200
TAAACTTACA TTTAGCTCAG TTTAATTACA GTCTTATTG GATGCATATG TATGGTTCTC	1260
AATCCATATA AGTTAGAGTA AAAAATAAGTTAAATTATA TCTTAATTCA CTCCAACATA	1320
TACGGATTGA GTACAATACT CATGTGCATC CAAACAAACT ACTTATATTG AGGTGAATT	1380
GGATAGAAAT TAAACTAACT TACACACTAA GCCAATCTTACTATATTAA AGCACCAGTT	1440
TCAACGATCG TCCCAGGTCA ATATTATTAA AAAACTCCTA CATTCTTTA TAATCAACCC	1500
GCACCTTAT AATCTCTTCT CTACTACTAT AATAAGAGAG TTTATGTACA AAATAAGGTG	1560
AAATTATGTA TAAGTGTCT GGATATTGGT TGTTAACTCC ATATTCACAC AACCTAATCA	1620
ATAGAAAACA TATGTTTAT TAAAACAAAA TTTATCATAT ATCATATATA TATATATACA	1680
TATATATATA TATATATATA TAAACCGTAG CAATGCACGG GCATATAACT AGTGCAACTT	1740
AATACATGTG TGTATTAAGA TGAATAAGAG GGTATCCAAA TAAAAAACTT GTTCGCTTAC	1800
GTCTGGATCA AATTGGTTG GAAACGATTA AATCTCTTCC TAGTCAAAAT TGAATAGAAG	1860
GAGATTTAAT CTCTCCCAAT CCCCTTCGAT CATCCAGGTG CAACCGTATA AGTCCTAAAG	1920
TGGTGAGGAA CACGAAACAA CCATGCATTG GCATGTAAAG CTCCAAGAAT TTGTTGTATC	1980
CTTAACAACT CACAGAACAT CAACCAAAAT TGCACGTCAA GGGTATTGGG TAAGAAACAA	2040
TCAAACAAAT CCTCTCTGTG TGCAAAGAAA CACGGTGAGT CATGCCGAGA TCATACTCAT	2100
CTGATATACA TGCTTACAGC TCACAAGACA TTACAAACAA CTCATATTGC ATTACAAAGA	2160

TCGTTTCATG AAAAATAAAA TAGGCCGGAC AGGACAAAAA TCCTTGACGA GTAAAGTAAA	2220
TTTACAACAA AAAAAAAGCC ATATGTCAAG CTAAATCTAA TTCGTTTAC GTAGATCAAC	2280
AACCTGTAGA AGGCAACAAA ACTGAGCCAC GCAGAAGTAC AGAATGATTC CAGATGAACC	2340
ATCGACGTGC TACGTAAAGA GAGTGACGAG TCATATACAT TTGGCAAGAA ACCATGAAGC	2400
TGCCTACAGC CGTCTCGGTG GCATAGGAAC ACAAGAAATT GTGTTAATTA ATCAAAGCTA	2460
TAAATAACGC TCGCATGCCT GTGCACTTCT CCATCACAC CACTGGGTCT TCAGACCATT	2520
AGCTTTATCT ACTCCAGAGC GCAGAAGAAC CCGATCGACA CCATGAGGGT GTTGCTCGTT	2580
GCCCTCGCTC TCCTGGCTCT CGCTGCGAGC GCCACCTCCA CGCATAACAG CGGGGGCTGC	2640
GGCTGCCAGC CACCGCCGCC GGTTCATCTA CCGCCGCCGG TGCATCTGCC ACCTCCGGTT	2700
CACCTGCCAC CTCCGGTGCA TCTCCCACCG CCGGTCCACC TGCCGCCGCC GGTCCACCTG	2760
CCACCGCCGG TCCATGTGCC GCCGCCGGTT CATCTGCCGC CGCCACCATG CCACTACCCT	2820
ACTCAACCGC CCCGGCTCA GCCTCATCCC CAGCCACACC CATGCCCGTG CCAACAGCCG	2880
CATCCAAGCC CGTGCCAGCT GCAGGGAACC TGCGCGTTG GCAGCACCCC GATCCTGGC	2940
CAGTGCCTCG AGTTCCTGAG GCATCAGTGC AGCCCGACGG CGACGCCCTA CTGCTCGCCT	3000
CAGTGCCAGT CGTTGCGGCA GCAGTGTTC CAGCAGCTCA GGCAGGTGGA GCCACAGCAC	3060
CGGTACCAGG CGATCTTCGG CTTGGTCCTC CAGTCCATCC TGCAGCAGCA GCCGCAAAGT	3120
GGCCAGGTGCG CGGGGCTGTT GGCGGCGCAG ATAGCGCAGC AACTGACGGC GATGTGCGGT	3180
CTGCAGCAGC CGACTCCATG CCCCTACGCT GCTGCCGGCG GTGTCCCCCA CTGAAGAAC	3240

TATGTGCTGT AGTATAGCCG CTGCCCGCTG GCTAGCTAGC TAGTTGAGTC ATTTAGCGGC	3300
GATGATTGAG TAATAATGTG TCACGCATCA CCATGGGTGG CAGTGTCACT GTGAGCAATG	3360
ACCTGAATGA ACAATTGAAA TGAAAAGAAA ATACTCCATC TGTTCCAAAT TAAAATTCCAT	3420
TTTAACCTTT TAATAGGTTT ATACAATAAT TGATATATGT TTTCTGTATA TGTCTAATT	3480
GTTATCATCC ATTTAGATAT AGACAAAAAA AAATCTAAGA ACTAAAACAA ATGCTAATT	3540
GAAATGAAGG GAGTATATAT TGGGATAATG TCGATGAGAT CCCTCGTAAT ATCACCGACA	3600
TCACACGTGT CCAGTTAATG TATCAGTGAT ACGTGTATTG ACATTTGTTG CGCGTAGGCG	3660
TACCCAACAA TTTTGATCGA CTATCAGAAA GTCAACGGAA GCGA	3704

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGCTCGAGTA AGTATGCAGG A	21
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(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGCTCGAGCA CTCGGCTTGC T

21

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGGGCTGATC CTGGCCGGCA CCGT

24

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTGTTCTCCT GGATGTACAA GTAC

24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCCAAGGCC GCGACGTCAA GGAAC

25